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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22 ; Search time 55:31:29 seconds
(without alignments) 11410 644 Million cell updates/sec

Title: perfect score: 26 US-OA-A10-428-1
Sequence: 1 qtgcctataattttctgttaccaag 26

Scoring table: IDENTITY_NUC
GapP 10 n GapExt 1 0
Searched: 2854640 seqs 14551402878 residues

Total number of hits satisfying chosen parameters: 4109290

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post processing Minimum Match %: 10.0%
Listing first 40 summaries:

Database :	GenBank:*	Result No.	Score	% Match	Length	DB ID	Description
1: qb_ba:*	1	25	100.0	34.9	4	AFL26288	AT12288 Bos tauru
2: qb_htg:*	2	26	100.0	7.2	4	AF00935	AC04055 Bos indic
3: qb_in:*	3	26	100.0	25688	4	BTM15731	U115731 Bos tauru
4: qb_om:*	4	19.8	76.2	126837	9	AL451106	AL451106 Human DNA
5: qb_ov:*	5	19.6	73.4	194427	2	AC04612	AC04612 Rattus no
6: qb_pn:*	6	19.6	75.4	193621	2	AC126834	AC126834 Rattus no
7: qb_sts:*	7	19.6	75.4	198624	2	AC01081	AC01081 Mus muscu
8: qb_sy:*	8	19.4	74.6	51881	9	AL158049	AL158049 Human DNA
9: qb_tg:*	9	19.2	73.8	115297	2	AC02077	AC02077 Homo sapien
10: qb_bt:*	10	19.2	73.8	153909	2	AC124782	AC124782 Rattus no
11: qb_bt:*	11	19.2	73.8	156042	2	AC125295	AC125295 Rattus no
12: qb_bt:*	12	19.2	71.8	160091	3	AC024242	AC024242 Human Chr
13: qb_bt:*	13	19.2	73.8	174776	9	AL19256	AL19256 Human DNA
14: qb_bt:*	14	19.2	73.8	187357	2	AC12988	AC12988 Rattus no
15: qb_bt:*	15	19.2	73.8	193446	2	AC034597	AC034597 Rattus no
16: qb_bt:*	16	18.8	72.3	89298	2	AC11858	AC11858 Mus muscu
17: qb_bt:*	17	18.8	72.3	121448	9	AC092659	AC092659 Homo sapi
18: qb_bt:*	18	18.8	72.3	155123	2	AC12447	AC12447 Rattus no
19: qb_bt:*	19	18.8	72.3	163246	2	AC07804	AC07804 Human DNA
20: qb_bt:*	20	18.8	72.3	193761	2	AC03223	AC03223 Homo sapien
21: qb_bt:*	21	18.8	72.3	188374	9	AC005050	AC005050 Homo sapi
22: qb_bt:*	22	18.8	72.3	190070	2	AC127907	AC127907 Rattus no
23: qb_bt:*	23	18.8	72.3	193305	2	AC030269	AC030269 Human DNA
24: qb_bt:*	24	18.8	72.3	194015	9	AC066612	AC066612 Rattus no
25: qb_bt:*	25	18.8	72.3	194324	2	AC039269	AC039269 Homo sapi
26: qb_bt:*	26	18.8	72.3	194360	2	AC039546	AC039546 Rattus no
27: qb_bt:*	27	18.8	72.3	207534	2	AC026598	AC026598 Homo sapi
28: qb_bt:*	28	18.6	72.3	190242	2	AC127907	AC127907 Rattus no
29: qb_bt:*	29	18.6	71.5	588	4	OAATPCP1	AC039269 Homo sapi
30: qb_bt:*	30	18.6	71.5	4669	10	AK01152	AC066612 Rattus no
31: qb_bt:*	31	18.6	71.5	17000	4	AK01152	AC066612 Rattus no
32: qb_bt:*	32	18.6	71.5	97037	9	AC034973	AC034973 Homo sapi
33: qb_bt:*	33	18.6	71.5	100165	2	AC103465	AC103465 Rattus no
34: qb_bt:*	34	18.6	71.5	102242	2	AP004043	AP004043 Oryza sativa
35: qb_bt:*	35	18.6	71.5	115846	2	AC104276	AC104276 Oryza sativa
36: qb_bt:*	36	18.6	71.5	128468	9	AL139090	AL139090 Human DNA
37: qb_bt:*	37	18.6	71.5	144174	2	AC119524	AC119524 Homo sapi
38: qb_bt:*	38	18.6	71.5	147765	2	AC004000	AC004000 Mus muscu
39: qb_bt:*	39	18.6	71.5	149094	2	AC116074	AC116074 Mus muscu
40: qb_bt:*	40	18.6	71.5	150354	2	AC00433	AC00433 Oryza sativa
41: qb_bt:*	41	18.6	71.5	157274	2	AP004679	AC004679 Human DNA
42: qb_bt:*	42	18.6	71.5	158966	2	AC011524	AC011524 Homo sapi
43: qb_bt:*	43	18.6	71.5	161520	4	AC110989	AC110989 Homo sapi
44: qb_bt:*	44	18.6	71.5	163498	2	AC127878	AC127878 Rattus no
45: qb_bt:*	45	18.6	71.5	166687	2	AC032236	AC032236 Homo sapi

ALIGNMENTS

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

pred. No. is the number of results predicted by chance to have a

RESULT 1
AF126288
FOCUS AF126288
DEFINITION Bos taurus growth hormone receptor (GHR) gene, promoter and untranslated region.
ACCESSION AF126288
VERSION AF12b88.1 61:4894683
KEYWORDS SOURCE
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Gartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 349)
AUTHORS Ge, W., Davis, M.E., Hines, H.C. and Ivin, K.M.

CDS
 /number="2
 25670...25688
 /node_start=1
 /product="Growth hormone regulator"
 /protein_id="ANK1298_1"
 /fth_xref="G1-1472479"
 /translation="M01NSC"

BASE COUNT
 ORIGIN
 6552 a 5982 c 6005 g 7149 t

Query Match 100.0% Score 26, DB 4, length 25688,

Best local Similarity 100.0% Pos. 0-24; Mismatches 0, Indels 0, Gaps 0;

Matches 26, Conservative 0, MisMatches 0, Indels 0, Gaps 0;

Q: 1 AGCTTATTAATTCTTACCCAGC 26
 Db 10109 GTCGTGTTAATTCTTCTTAAAGC 10134

RESULT 4

ALL451106 A:451106
 LENGTH 125457 bp DNA Linear FPL 24-SEP-2001

DEFINITION Human DNA sequence from N_A_451106 FPL:151K-0-1353-94 X-0-X112
 Contains the 5' end of the ARHGAP gene for sub 42 gata-binding exchange factor 9 (GBF1) cDNA. FPL 2. HPEM 2. KIAA0121) FSSS, GSSS and a CPG island, complete sequence.

ACCESSION A2451106
 VERSION A2451106_9 GR:1480108

KEYWORDS HPE, ARHGAP, cyclinB1, GPF, island, GFP, HPEM 2, KIAA0124, PEM-2, human.

SOURCE
 ORGANISM Homo sapiens
 Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

REFERENCE LITTLE JOURNAL
 Submitted (24 SEP 2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail: enquiries@sanger.ac.uk clone 1 (bases 1 to 126837)
 Whitehead, S.

COMMENT On Jul 17, 2001 this sequence version replaced 3:13751499 during sequence assembly data is compared from overlapping clones. Where differences are found those are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either shotgun-sequenced or subjected with an alternative chemistry or covered by high quality data (i.e., Phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases. Em., EMBL, Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/Celegans/wormpep>. Information on the WORMPEP database was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/Projects/X/ChX>. RP11-151A2 is from the library FPL 11.1 constructed by the group of Peter de Jong. For further details see <http://www.sanger.ac.uk/Chapman/>.

sections only once, except for a short overlap. The true left end of clone RP11-151A2 is at 1 in this sequence. The true left end of clone RP11-56920 is at 126738 in this sequence.

location/Qualifiers 1..126837

/organism="Homo sapiens"

/db_xref="Taxon:9606"

/chromosome="X"

/fseq="FPL1151A2"

/clone_id="RPCI-11-1"

/note="match: GSS: Em:AQ377441"

/repeat_region 2543..2601

/note="MR repeat, matches 31..85 of consensus"

/repeat_region 2723..2773

/note="MR repeat, matches 71..131 of consensus"

/repeat_region 3442..3709

/note="Arf5x repeat, matches 2..352 of consensus"

/repeat_region 3517..4342

/note="match: GSS: Em:AY242430"

/repeat_region 3522..4001

/note="match: GSS: Em:AU255552"

/repeat_region 3523..3931

/note="match: GSS: Em:AU37685"

/repeat_region 3608..3696

/note="match: GSS: Em:AU37655"

/repeat_region 3698..3970

/note="match: GSS: Em:AU098555"

/repeat_region 4392..4882

/note="match: GSS: Em:AY29761"

/repeat_region 4616..4572

/note="L2 repeat, matches 2652..2708 of consensus"

/repeat_region 4823..4926

/note="MER repeat, matches 45..146 of consensus"

/repeat_region 6055..6155

/note="MER repeat, matches 36..146 of consensus"

/repeat_region 673..7755

/note="MER repeat, matches 63..148 of consensus"

/repeat_region 8033..8210

/note="MER5B repeat, matches 1..178 of consensus"

/repeat_region 8900..9001

/note="MER repeat, matches 108..938 conserved"

/repeat_region 9109..9293

/note="MER5B repeat, matches 8..175 of consensus"

/repeat_region 9709..10017

/note="AluSS repeat, matches 1..310 of consensus"

/repeat_region 10109..10200

/note="MER repeat, matches 106..132 of consensus"

/repeat_region 12845..12890

/note="18 copies 2 mer aa 86% conserved"

/repeat_region complement(14719..15600)

/note="Arf5x repeat, matches 1..42 gata-binding exchange factor (GBF) 9

/product="BAF151A2-1 (Cdc42 gata-binding exchange factor (GBF) 9 cyclinB1, HPEM-2, HPEM-1, KIAA0124)"

/note="continues as BA570118_1.mRNA in Em:AL351142 and BA35102_2.mRNA in Em:AL392277"

/match: CDNAS: Em:AB007884

/evidence-not_experimental Evidence-not_experimental

IMPORTANT: This sequence is not the entire insert of clone RP11-151A2. It may be shorter because we sequence overlapping

COMMENT

On Dec 20, 2001 this sequence version replaced g1:15624447.

..... Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.bmc.brown.edu/edj/

Contact: bmc@bcm.edu

Center project name: GBAJ

Project Information

Center clone name: GBAJ

Summary Statistics

Assembly program: Phrap; version 0.990329first; call to

findphraplist

* NOTE: Estimated insert size may differ from sequence length.

* (see http://www.bmc.brown.edu/edj/GbankDraftData.html)

* NOTE: This is a 'working draft' sequence. It currently

* consists of 59 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1 9929: contig of 9929 bp in length

2 9930: 10029: gap of unknown length

3 10030: 10562: contig of 9513 bp in length

4 19563: 19662: gap of unknown length

5 19663: 20954: contig of 6292 bp in length

6 20954: 2055: gap of unknown length

7 31955: 32054: contig of 5900 bp in length

8 32054: 38436: gap of unknown length

9 38436: 38536: gap of unknown length

10 38536: 42643: contig of 4107 bp in length

11 42643: 42743: gap of unknown length

12 42743: 42744: contig of 4938 bp in length

13 42744: 47882: gap of unknown length

14 47882: 51504: contig of 3723 bp in length

15 51504: 51604: gap of unknown length

16 51604: 54660: contig of 3056 bp in length

17 54660: 54760: gap of unknown length

18 54760: 54761: contig of 5130 bp in length

19 54761: 58990: gap of unknown length

20 58990: 59390: gap of unknown length

21 59390: 63789: gap of unknown length

22 63789: 66937: contig of 3208 bp in length

23 66937: 67098: gap of unknown length

24 67098: 70030: contig of 2933 bp in length

25 70030: 70310: gap of unknown length

26 70310: 74162: contig of 4032 bp in length

27 74162: 74262: gap of unknown length

28 74262: 77599: contig of 3337 bp in length

29 77599: 77600: gap of unknown length

30 77600: 79923: contig of 2224 bp in length

31 79923: 80223: gap of unknown length

32 80223: 80714: contig of 2276 bp in length

33 80714: 82449: gap of unknown length

34 82449: 82650: contig of 2371 bp in length

35 82650: 85021: gap of unknown length

36 85021: 85121: contig of 3543 bp in length

37 85121: 88664: gap of unknown length

38 88664: 88763: gap of unknown length

39 88763: 91498: gap of unknown length

40 91498: 91549: contig of 1542 bp in length

41 91549: 93240: gap of unknown length

42 93240: 95402: contig of 2063 bp in length

43 95402: 95503: gap of unknown length

44 95403: 98038: contig of 2636 bp in length

45 98038: gap of unknown length

46 98139: contig of 4051 bp in length

47 101199: gap of unknown length

48 102200: contig of 1715 bp in length

49 105343: contig of 3044 bp in length

50 105444: gap of unknown length

51 108005: contig of 2562 bp in length

52 108006: gap of unknown length

53 109821: contig of 1794 bp in length

54 112015: gap of 2094 bp in length

55 112015: gap of unknown length

56 112115: gap of 2183 bp in length

57 114298: gap of unknown length

58 114397: contig of 1537 bp in length

59 114655: gap of unknown length

60 114754: contig of 1803 bp in length

61 116300: gap of unknown length

62 118540: contig of 1286 bp in length

63 118541: gap of unknown length

64 120017: contig of 1377 bp in length

65 120018: gap of unknown length

66 12114: gap of 2106 bp in length

67 123345: gap of unknown length

68 123345: contig of 2591 bp in length

69 123737: gap of unknown length

70 127938: contig of 1924 bp in length

71 127938: gap of 1928 bp in length

72 129965: contig of unknown length

73 129966: gap of unknown length

74 130056: 131785: contig of 1720 bp in length

75 130056: 131785: gap of unknown length

76 131786: 131885: gap of unknown length

77 131786: 131885: contig of 2440 bp in length

78 13325: 134325: gap of unknown length

79 134426: 134426: contig of 1924 bp in length

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177 134426: 134426: contig of 1924 bp in length

LOCUS	ACCESSION	DEFINITION	COMMENT
49197	49296	gap of unknown length	198624 bp DNA linear uncloned
* 49297	57707	contig of 241 bp in length	uncloned
* 51708	51807	gap of unknown length	Mus musculus clone KU23-387k-3, working draft sequence, 8 unordered pieces.
* 51808	54110	contig of 2303 bp in length	AC101881.2
* 54210	54211	gap at unknown length	AC101881.3 GI:22381426
* 54211	57375	contig of 3165 bp in length	KEYWORDS
* 57376	57475	gap of unknown length	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
* 57476	60536	contig of 3061 bp in length	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
* 60537	60636	gap of unknown length	1 (bases 1 to 198624)
* 63317	63318	contig of 2681 bp in length	AUTHORS
* 63417	63418	gap of unknown length	Birren, B., Nusbaum, C. and Lander, E.
* 63418	65968	contig of 2551 bp in length	TITLE
* 65968	66068	gap of unknown length	Mus musculus, clone RP23-387f19
* 66069	69498	contig of 3430 bp in length	SOURCE
* 69499	69598	gap of unknown length	Unpublished
* 69599	71526	contig of 1928 bp in length	JOURNAL
* 71527	71626	gap of unknown length	2 (bases 1 to 198624)
* 71627	74676	contig of 3050 bp in length	AUTHORS
* 74677	74776	gap of unknown length	Birren, B., Linton, L., Nusbaum, C., Lander, E., Alia, A., Allen, N.,
* 74777	77583	contig of 2867 bp in length	Audretsch, S., Barna, N., Bastien, V., Boisclair, Y., Boukhvalter, B.,
* 77584	77683	gap of unknown length	Chechet, N., Cuijana, P., Campobolo, A., Chang, J., Chataro, H.,
* 77684	80148	contig of 2465 bp in length	Corvera, M., DeArdo, J., DeWitt, K., Diaz, J. S., Dudoit, S., Faro, S.,
* 80149	80248	gap of unknown length	Ferreira, P., FitzHugh, W., Gage, D., Galaz, J., Gardyna, S.,
* 80249	82557	contig of 2309 bp in length	Ginde, S., Gord, S., Goylette, M., Graham, L., Grand-Pierre, N.,
* 82558	82557	gap of unknown length	Hagos, B., Heaford, A., Horton, L., Huime, W., Iliev, I., Johnson, R.,
* 82658	84181	contig of 1824 bp in length	Jones, C., Kamat, A., Karatas, A., Keil, S., LaRocque, K.,
* 84181	84481	gap of unknown length	Lazarev, R., Landers, T., Lebowitz, J., Levine, R., Liu, G.,
* 84482	87302	contig of 2721 bp in length	MacLeath, C., MacLoud, P., Major, J., Marquis, N., Matthews, C.,
* 87303	87403	gap of unknown length	McCarthy, M., McEwan, P., McKernan, K., Melidris, J.,
* 87403	90698	contig of 3295 bp in length	Moneus, L., Mitova, T., Mienga, V., Murphy, T., Nayak, J., Nguyen, G.,
* 90698	93986	gap of unknown length	Norbu, C., Norman, C. H., O'Conor, T., O'Donnell, P., O'Neil, D.,
* 93987	94086	contig of 3189 bp in length	Oliver, J., Peterson, K., Punckhang, P., Pieret, N., Pollara, V.,
* 94087	97550	contig of 3464 bp in length	Purdon, C., Rettar, R., Riback, M., Riley, K., Rice, C., Rogov, P.,
* 97551	10273	gap of unknown length	Roman, J., Rosetti, J., Roy, A., Santos, R., Schauer, S., Schupback, R.,
* 10273	105268	contig of 2895 bp in length	Seaman, S., Severy, P., Spencer, B., Staine-Thomann, N., Stolano-N.,
* 105169	109192	gap of unknown length	Strauss, N., Subramanian, A., Talamas, J., Testayre, S., Theodore, J.,
* 109193	109292	gap of unknown length	Topham, K., Travers, M., Travis, N., Triplillo, T., Vassiliev, N.,
* 109293	114339	contig of 5047 bp in length	Wei, R., Yel, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
* 114340	114349	gap of unknown length	Zainoun, J., Zentek, B., Zimmer, A. and Zody, M.
* 114440	118203	contig of 3668 bp in length	Direct Submission
* 118208	122052	gap of unknown length	Submitted [23-NOV-2001] Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
* 122753	122752	contig of 4445 bp in length	REFERENCE
* 122753	128244	gap of unknown length	AUTHORS
* 128244	128425	contig of 5088 bp in length	Birren, B., Nusbaum, C., Landers, T., All, A., Allen, N., Anderson, S.,
* 133513	133612	gap of unknown length	Barnai, N., Bastien, V., Bloom, T., Boguslavsky, I., Boukhalter, B.,
* 133613	14118	contig of 7706 bp in length	Camarra, J., Chang, J., Charo, B., Chechet, N., Collymore, A.,
* 14119	141418	gap of unknown length	Cook, A., Corke, P., DeAngelis, K., Dewar, K., Diaz, J. S., Dodge, S.,
* 141419	147572	contig of 6154 bp in length	Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galaz, J.,
* 147572	147572	gap of unknown length	Gardita, S., Giudice, S., Graham, J., Grand-Pierre, N., Hagos, B.,
* 147573	147573	contig of 7975 bp in length	Horton, J., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
* 147573	155648	gap of unknown length	Karatas, A., Keil, S., Landers, T., Levine, R., Lindblad-Toh, K.,
* 155747	155747	gap of unknown length	Liu, G., MacLean, C., MacLoud, P., Major, J., Matthews, C.,
* 155748	163030	contig of 7283 bp in length	McCarthy, M., McEwan, P., Meneus, L., Mitova, T., Mienga, V.,
* 163031	163140	gap of unknown length	Murphy, T., Nayak, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
* 163140	173435	contig of 10305 bp in length	O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Purdon, C., Rettar, R., Riback, M., Riley, K., Rice, C., Rogov, P.,
* 173435	173436	gap of unknown length	Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomas, N., Stojanovic, N., Talamas, J., Testayre, S., Theodore, J., Topham, K., Travers, M., Vassiliev, N., Vieil, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zentek, B., Zimmer, A. and Zody, M.
* 173436	173436	contig of 10305 bp in length	TITLE
* 173436	173436	gap of unknown length	Internal
* 173436	173436	contig of 10305 bp in length	RESEARCH
* 173436	173436	gap of unknown length	On Aug 21, 2002 this sequence was last updated at 17060657.
* 173436	173436	contig of 10305 bp in length	All repeats were identified using RepeatMasker.
* 173436	173436	gap of unknown length	Smith, A.P.A. & Green, P. (1996-1997)
* 173436	173436	contig of 10305 bp in length	http://fti.genome.wustl.edu/pmcaserver.html
* 173436	173436	gap of unknown length	Project information
* 173436	173436	contig of 10305 bp in length	Center Project name: L17690

Query Match Score 196 DR 2 length 183621:
 Best Local Similarity 84.6% Pred. No. 1.7e-02; Mismatches 22;保守性 0; Indels 0; Gaps 0;

QY 1 CGCCGAACTTCTTGATCAGG 26
 Db 80065 SGCTTAATCTCTGGATCAGG 80040

RESULT 7
 AC101881/c

ordered piece.

ACCESSION U82207
VERSION U82207_1_GI_3983519

KEYWORDS HTGS_PHASE2; HTGS_CANCELLED.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

JOURNAL Eukaryota; Metazoa; chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 115297)

AUTHORS Smith,D.R.

TITLE Sequencing of Human Chromosome 19

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 115297)

AUTHORS Burd,J. and Smith,D.

JOURNAL Direct Submission

COMMENT Submitted (13-Dec-1996) Bioinformatics revision. Genome Therapies Corporation Inn Bayview Street, Waltham, MA 02154, USA

Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing technology. Data may contain low quality sequence and BAC assembly vector sequences.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given; however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter

* this sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 115297: contig of 115297 bp in length.

FEATURES source

1. 115297

/clone=CIT997SK-1119P3*

/chromosome="10"

/map="10q25.1"

/db_xref="taxon:9606"

RAPE COUNT 11990

ORIGIN 22267 23595 3 35055 t

RHSLP 10

AC124782 AC124782

DEFINITION Rattus norvegicus clone CIRP044703, *** SEQUENCING IN PROGRESS

QY 1 GGCGCTAAATTTCCTTGTACCA 24

Db 99505 (RNU19A)RATTTCCTTGTACCA 9448?

ORGANISM Rattus norvegicus

Query Match 73 8%; Score 19 2; DB 2; Length 115297;

Matches 21; Conserva, ave 0; Mismatches 3; Indels 0; Gaps 0;

COMMENT

ACCESSION AC124782

DEFINITION Rattus norvegicus clone CIRP044703, *** SEQUENCING IN PROGRESS

VERSION AC124782

KEYWORDS HTGS_PHASE1

SOURCE Norway rat

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 154909)

AUTHORS Muzny,D.M., Adams,C., Adio-Oduua,B., Alfonsoan,F.R., Allen,C., Alsbrooks,S.L., Amaralungu,H.C., Are,J.R., Ayotte,M., Banks,T., Barbara,J., Benton,T., Blainage,K., Blatnerburg,K., Bonin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,F.L., Byrd,N.C., Carron,T.F., Carrier,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chodhury,I., Christopoulos,C., Cleveland,C.C., Cox,C.C., Coyle,M.D., Dabholkar,S.R., David,R., Davila,M.L., Davis,C., Davy Carroll,L., Dederich,D.A.,

Delaney,K.R., Delgado,O., Dent,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,B., Duncan-Rocha,S., Durbin,K.J., Earnhardt,C., Edgar,D., Edwards,C.C., El Hajj,C., Escoffre,M., Fallis,T., Ferradou,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gorrell,J.H., Guvara,W., Guiratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A., Hernandez,J., Hernandez,O., Hodges,A., Hoque,M., Holloway,C., Hollins,B., Homsi,R., Howard,S., Huber,J.J., Hulk,S., Huie,J., Jackson,J.E., Jacobson,B., Jia,Y., Johnson,K., Jolivet,S., Joukah,S., Karlsson,J., Keily,S., Khatri,U., Kishin,K., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Liu,X., Lucier,A., Lucier,R., Tuna,R., Lui,J., Liu,W., Louiseau,H., Lorado,R.J., Lu,X., Lucier,A., Lucier,R., Tuna,R., Ma,J., Mabashira,I., Mapua,R., Martin,P., Martindale,A., Martinez,R., Maser,M., Minet,J., Mitchell,T., Mohabat,K., Muigai,M., Mullis,S., Muster,M., Neal,D., Newston,J., Newston,R., Nguyen,N., Nguyen,N., Nickerson,E., Nwokonkwo,S., Oquih,M., Okwundu,G., Crazeane,N., Oviedo,R., Pacer,J., Partron,B., Peery,J., Perez,L., Peters,J., Pickens,R., Primus,E., Putt,L., Quiles,M., Ron,Y., Rives,M., Rojas,A., Rojubon,J., Roit,M., Ruiz,S., Savory,G., Scherer,S., Scott,G., Shen,H., Shoultz,N., Sison,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tammerka,K., Tang,H., Tarsue,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,J., Veta,J., Villalon,M., Visson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wieczork,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zourilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 153909)

Worley,K.C.

JOURNAL Direct Submission

COMMENT Submitted (17-JUN-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, one

3 (bases 1 to 153909)

Worley,K.C.

JOURNAL Direct Submission

COMMENT Submitted (11-JUL-2002) Human Genome Sequencing center, Department

of Molecular and Human Genetics, Baylor College of Medicine, one

3 (bases 1 to 153909)

Worley,K.C.

JOURNAL Direct Submission

COMMENT Submitted (11-JUL-2002) Human Genome Sequencing center, Department

of Molecular and Human Genetics, Baylor College of Medicine, one

3 (bases 1 to 153909)

Worley,K.C.

JOURNAL Direct Submission

COMMENT Submitted (11-JUL-2002) Human Genome Sequencing center, Department

of Molecular and Human Genetics, Baylor College of Medicine, one

3 (bases 1 to 153909)

Worley,K.C.

JOURNAL Direct Submission

COMMENT Submitted (11-JUL-2002) Human Genome Sequencing center, Department

of Molecular and Human Genetics, Baylor College of Medicine, one

3 (bases 1 to 153909)

Worley,K.C.

JOURNAL Direct Submission

COMMENT Submitted (11-JUL-2002) Human Genome Sequencing center, Department

of Molecular and Human Genetics, Baylor College of Medicine, one

3 (bases 1 to 153909)

Worley,K.C.

JOURNAL Direct Submission

COMMENT Submitted (11-JUL-2002) Human Genome Sequencing center, Department

of Molecular and Human Genetics, Baylor College of Medicine, one

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JOURNAL Direct Submission

COMMENT Submitted (11-JUL-2002) Human Genome Sequencing center, Department

of Molecular and Human Genetics, Baylor College of Medicine, one

3 (bases 1 to 153909)

Worley,K.C.

JOURNAL Direct Submission

COMMENT Submitted (11-JUL-2002) Human Genome Sequencing center, Department

of Molecular and Human Genetics, Baylor College of Medicine, one

3 (bases 1 to 153909)

Worley,K.C.

1163 1262: qap of unknown length
1263 2412: contig of 1150 bp in length
2413 2512: qap of unknown length
2513 5048: contig of 2546 bp in length
5049 5148: qap of unknown length
5149 6814: contig of 1666 bp in length
6815 6914: qap of unknown length
6915 8702: contig of 1788 bp in length
8703 8802: qap of unknown length
8803 10386: contig of 1584 bp in length
10387 10486: qap of unknown length
10487 12877: contig of 2490 bp in length
12877 12976: qap of unknown length
12977 15600: contig of 2624 bp in length
15601 15700: qap of unknown length
15701 15772: contig of 2072 bp in length
15773 17872: qap of unknown length
17873 19852: contig of 1980 bp in length
19853 19952: qap of unknown length
19953 22945: contig of 2994 bp in length
22946 23045: qap of unknown length
23046 26798: contig of 3753 bp in length
26799 26898: qap of unknown length
26899 29328: contig of 2430 bp in length
29429 29428: qap of unknown length
29429 32779: contig of 3351 bp in length
32780 32879: qap of unknown length
32880 35857: contig of 2179 bp in length
35058 35157: qap of unknown length
35158 37481: contig of 2324 bp in length
37482 37581: qap of unknown length
37582 39870: contig of 2289 bp in length
39871 43970: qap of unknown length
43971 44218: contig of 2215 bp in length
44218 44285: qap of unknown length
44286 44726: contig of 2441 bp in length
44727 44826: qap of unknown length
44827 47837: contig of 3011 bp in length
47838 47937: qap of unknown length
51213 51213: contig of 3237 bp in length
51213 51312: qap of unknown length
51313 57141: contig of 5819 bp in length
57142 57231: qap of unknown length
57232 61394: contig of 4163 bp in length
61395 61494: qap of unknown length
61495 65007: contig of 3514 bp in length
65007 65107: qap of unknown length
65107 69017: contig of 3910 bp in length
69018 69117: qap of unknown length
69118 74160: contig of 4033 bp in length
74161 74260: qap of unknown length
74261 79804: contig of 6543 bp in length
79804 79904: qap of unknown length
79904 84613: contig of 4710 bp in length
84614 84714: contig of unknown length
84714 90271: contig of 5758 bp in length
90272 90371: qap of unknown length
90372 95107: contig of 4746 bp in length
95108 95207: qap of unknown length
95208 190696: contig of 5489 bp in length
190697 100697: contig of unknown length
100697 100797: contig of 7340 bp in length
100797 108127: qap of unknown length
108127 108226: contig of 5048 bp in length
108227 115091: contig of 6865 bp in length
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115192 122209: contig of 7018 bp in length
122209 122309: contig of unknown length
122309 122410: qap of unknown length
122410 128944: contig of 6625 bp in length
128945 129034: qap of unknown length
129035 134182: contig of 5048 bp in length
134183 142165: contig of 7948 bp in length
142165 142265: qap of unknown length

FEATURES	*	142266	153909: contig of 11644 bp in length.
SOURCE			location/qualifiers
QY	3	GCCTCAATTCCTTGGTAGGAGG	score 19.2, db 27; Length 154909;
Db	152732	GCTCTAATCTTACTACATG	best Local Similarity 87.5%; Fred. No. 2, 6e-02; Matches 21, Conservativeness 0.5, Mismatches 3, Indexes 6, Status 0;
BASE COUNT	43135	a 32216 c 30384 g 43273 t 4901 others	ORIGIN
RESULT	11		
AC125295			
Locus	AC125295	156045 bp DNA	linear
DEFINITION		59 unordered pieces.	HTS 11 SLL 2002
ACCESSION	AC125295		
VERSION	AC125295.1	C1-21539019	
KEYWORDS	HIGS_PHASE1		
SOURCE	Norway rat		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurognathia; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 156042)		
AUTHORS	Muzny, D.M., Adams, S., Adio, Oñate, B., Ali, Osman, F.R., Allen, C., Alshabani, S.L., Amarasinghe, H.C., Are, J.R., Ayotte, M., Banks, T., Barron, J., Bentzen, J., Bingham, K., Blankenburg, K., Bonotto, D., Bouck, J., Bowie, S., Briceva, M., Brown, K., Brown, M., Bryant, N.P., Buray, C., Burton, P., Burkett, C., Burrell, K., Byrd, N.C., Carron, T., Carter, M., Cavazos, S.R., Chakraborty, J., Chavez, D., Chen, G., Chen, R., Chin, Z., Chowdhury, I., Christopoulos, G., Cleveland, G., Cui, Q., Cui, Q., Cox, M.D., Dabholkar, S., David, R., Dabney, K.R., Delgado, O., Deneen, A.L., Ding, Y., Dinh, H.H., Douthaito, K.J., Draper, H., Dugan-Rothka, S., Durkin, K.J., Farmar, C., Edgar, D., Edwards, C.C., Elhai, C., Escorcia, M., Falls, T., Ferragut, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabi, A., Gao, J., Garscia, A., Garner, L., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Guiralane, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J., Hertz, D., Hodges, A., Hopkins, A., Hough, C., Hollings, B., Homsi, F., Howard, S., Huber, J.J., Holly, S., Jackson, J., Jackson, B., Jia, Y., Johnson, R., Jolivet, S., Joudan, S., Karlsson, E., Kelly, S., Khan, U., Lin, Z., Lovelock, J., Mayar, G., Kratochvík, J., Kureishi, A., Landry, N., Leal, B., Lewis, L.G., Lewis, S., Li, J., Li, Z., Libetarique, O., Liu, C., Liu, J., Liu, W., Louisjeed, H., Lozada, R.J., Lu, X., Luytje, A., Macias, R., Jana, R., Ma, J., Maheshwari, M., Maior, P., Martin, R., Martindale, A., Martinez, R., Masser, E., Masterson, E., McDonald, M., McNeair, M., McNeil, G., McRae, M., Miner, G., Mirav, Z., Mitra, B., Molabolot, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newson, J., Newtonson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerison, E., Novakenko, S., Oquih, M., Okamoto, G., Oranuyan, N., Owicki, C., Pace, R., Payton, B., Peery, A., Peters, B., Pickens, R., Primus, B., Purnell, J., Quilles, M., Reilly, W., Rivers, M., Rajas, A., Rojek, J., Rolfe, M., Ross, S., Sastry, G., Scheerer, S., Scott, G., Shen, H., Shospisari, N., Sisson, T., Sodergreen, E., Sonnake, T., Sparks, A., Stanley, B., Stone, H., Sutton, A., Svatek, A., Taylor, P., Taudela, A., Tautz, I., Tautz, J., Tautz, K., Tautz, S., Tautz, T., Tautz, V., Thomas, N., Thomas, S., Usmani, R., Vasquez, L., Veray, V., Villalon, D., Vinson, R., Wan, Q., Wang, S., Ward, Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wilezyk, R., Warden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weintraub, G., and Gibbs, R.		
TITLE	Direct Submission		

JOURNAL: Unpublished
 REFERENCE: 2 (bases 1 to 156042)
 AUTHORS: Worley, K.C.
 TITLE: Direct Submission
 JOURNAL: submitted (22-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 COMMENT: 3 (bases 1 to 156042)
 PREFERENCE: Direct Submission
 JOURNAL: Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 CENTER: Baylor College of Medicine
 CENTER CODE: BCM
 CONTACT: hgsc@bcm.edu
 WEB SITE: http://www.hgsc.bcm.edu/
 CENTER PROJECT NAME: GRCI
 CENTER CLONE NAME: CH230-9A11
 SEQUENCING VECTOR: Plasmid
 CHEMISTRY: dye terminator, Big Dye, 100% of reads
 ASSEMBLY PROGRAM: phrap, version 0.990329
 CONSENSUS QUALITY: 110586 bases at least Q40
 CONSENSUS QUALITY: 11829 bases at least Q30
 CONSENSUS QUALITY: 119348 bases at least Q20
 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.edu/sequencing/submit_data.html)
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 59 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 1 1007: contig of 1007 bp in length
 * 1107: gap of unknown length
 * 1108: 2347: contig of 1240 bp in length
 2348: 3631: contig of 1184 bp in length
 * 3632: 3731: gap of unknown length
 * 3732: 4971: contig of 1240 bp in length
 4972: 5071: gap of unknown length
 * 5072: 6292: contig of 1221 bp in length
 * 6293: 6322: gap of unknown length
 * 6393: 8136: 8235: gap of unknown length
 * 8236: 9890: contig of 1445 bp in length
 * 9891: 10866: contig of 1086 bp in length
 * 10867: 12155: gap of unknown length
 * 12556: 14236: contig of 1371 bp in length
 * 14337: 15527: contig of 1231 bp in length
 * 15528: 15637: gap of unknown length
 * 15638: contig of 1789 bp in length
 * 15639: 16608: contig of 1041 bp in length
 * 16669: 16758: gap of unknown length
 * 16769: 18055: contig of 177 bp in length
 * 18056: 18605: gap of unknown length
 * 18606: 19771: contig of 1166 bp in length
 * 19772: 19871: gap of unknown length
 * 19872: 20934: contig of 1083 bp in length
 * 20935: 21044: gap of unknown length
 * 21055: 23216: contig of 2161 bp in length
 * 23316: 24710: contig of 195 bp in length
 * 24701: 24890: gap of unknown length
 * 24891: 25086: contig of 1186 bp in length
 * 25087: 26086: gap of unknown length
 * 26087: 26532: gap of 1546 bp in length
 * 27633: 27732: gap of unknown length
 * 27733: 27721: contig of 1989 bp in length
 * 29722: 29921: gap of unknown length
 * 29922: 31291: contig of 1470 bp in length
 * 31292: 31391: gap of unknown length
 * 31392: 33459: contig of 2068 bp in length
 * 33460: 33559: gap of unknown length
 * 33560: 34894: contig of 1335 bp in length
 * 34895: 34994: gap of unknown length
 * 34995: 36116: contig of 1121 bp in length
 * 36116: 36215: gap of unknown length
 * 36215: 37967: contig of 1752 bp in length
 * 37968: 38067: gap of unknown length
 * 38067: 40868: contig of 2800 bp in length
 * 40868: 40967: gap of unknown length
 * 40967: 42700: contig of 1733 bp in length
 * 42700: 42801: gap of unknown length
 * 42801: 45131: contig of 2331 bp in length
 * 45131: 45231: gap of unknown length
 * 45231: 45332: contig of 3037 bp in length
 * 45332: 48268: contig of 3015 bp in length
 * 48268: 48369: gap of unknown length
 * 48369: 50510: contig of 2142 bp in length
 * 50510: 50611: gap of unknown length
 * 50611: 50810: contig of 1996 bp in length
 * 50810: 52607: gap of unknown length
 * 52607: 52706: gap of unknown length
 * 52706: 55721: contig of 3015 bp in length
 * 55721: 55722: gap of unknown length
 * 55722: 55723: contig of 2588 bp in length
 * 55723: 58410: gap of unknown length
 * 58410: 58509: gap of unknown length
 * 58509: 58606: contig of 3123 bp in length
 * 58606: 61633: gap of unknown length
 * 61633: 61732: gap of unknown length
 * 61732: 64089: contig of 2357 bp in length
 * 64089: 64190: gap of unknown length
 * 64190: 66334: contig of 2445 bp in length
 * 66334: 66734: gap of unknown length
 * 66734: 66919: contig of 3085 bp in length
 * 66919: 69820: gap of unknown length
 * 69820: 71224: contig of 2305 bp in length
 * 71224: 72225: gap of unknown length
 * 72225: 75541: contig of 3317 bp in length
 * 75541: 75742: gap of unknown length
 * 75742: 77542: contig of 2244 bp in length
 * 77542: 77786: gap of unknown length
 * 77786: 78085: contig of 2724 bp in length
 * 78085: 78089: contig of 3361 bp in length
 * 78089: 80809: gap of unknown length
 * 80809: 86316: contig of 2191 bp in length
 * 86316: 86916: gap of unknown length
 * 86916: 88919: contig of 2670 bp in length
 * 88919: 92389: gap of unknown length
 * 92389: 92489: contig of 1571 bp in length
 * 92489: 94059: contig of 3257 bp in length
 * 94059: 94060: gap of unknown length
 * 94060: 94159: contig of 3361 bp in length
 * 94159: 94160: gap of unknown length
 * 94160: 95752: contig of 3341 bp in length
 * 95752: 97501: gap of unknown length
 * 97501: 100607: contig of 2807 bp in length
 * 100607: 100507: gap of unknown length
 * 100507: 100508: gap of unknown length
 * 100508: 100939: contig of 3432 bp in length
 * 100939: 104039: gap of unknown length
 * 104039: 104140: gap of unknown length
 * 104140: 104632: contig of 4223 bp in length
 * 104632: 108412: gap of unknown length
 * 108412: 108413: contig of 3769 bp in length
 * 108413: 112122: gap of unknown length
 * 112122: 112223: gap of unknown length
 * 112223: 115704: contig of 3483 bp in length
 * 115704: 115705: gap of unknown length
 * 115705: 115708: contig of 6224 bp in length
 * 115708: 122559: gap of unknown length
 * 122559: 122558: gap of unknown length
 * 122558: 122559: contig of 4569 bp in length

RESULT 14	AC129388	Rattus norvegicus	187357 bp	DNA	Library	HIG 23	PCR 30002
LOCUS							
DEFINITION		Rattus norvegicus clone CH20 3GB	*** Sequencing in progress ***				
ACCESSION	AC129388						
VERSION	1	GI 22021459					
KWYWORDS	HTCS_PHRSEI						
SOURCE	Rattus norvegicus						
ORGANISM	Rattus norvegicus						
REFERENCE							
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus						
1 (bases 1 to 187357)							
Muzny, D.M., Adams, M.D., Abood, S., Alu-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.J., Amaratunge, H.C., Are, J.R., Ayotte, M., Banks, T., Bartak, J., Bechtel, J., Bilezikian, K., Blautkeburg, B., Boultbee, D., Bough, M., Brown, M., Brown, N., Breyant, N.P., Buck, J., Buhler, S., Briceva, M., Brown, K., Buitenkamp, B., Buitenhuis, B., Burch, P., Burkett, C., Burrell, V., Byrd, N.C., Carron, T., Carter, M., Cavadas, S., Charkiewicz, J., Chavez, E., Chen, G., Chen, R., Chen, Z., Cheung, Y., Christopoulos, C., Cleverly, J., Cohn, C., Cui, M.C., Cuthbertson, S.E., Davy, G., Davis, C., Davis-Carroll, J., DeBenedictis, D.A., Delaney, K.R., Delgado, O., Denin, A.I., Ding, M., Dinn, H.H., Hernandez, G., Head, J., Heidmann, A., Higgins, M., Hinshaw, J., Hollingshead, B., Homsi, F., Howard, S., Hunter, R., Holly, S., Horne, T., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Toliver, S., Touzah, S., Karlsund, K., Kelly, S.V., Khan, U., King, L., Korwaj, J., Kovari, C., Kratochvili, J., Kuroki, A., Landry, N., Leal, B., Lewish, C., Lewis, L., Li, J., Li, Z., Lichagor, O., Lieu, C., Liu, J., Liu, W., Ioultsed, H., Lozano, R.J., Lu, X., Lucifer, A., Lucifer, R., Luna, R., Ma, J., Maheshwari, M., Marfa, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meadow, M., Meij, G., Metzker, M., Miner, G., Minetto, M., Mitchell, J., Molakatkar, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtonson, J., Newtonson, N., Nguyen, A., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, R., Nwokonkwo, S., Oghuh, M., Okwonwu, G., Oraquaye, N., Ouellet, P., Parra, A., Payrin, T., Perry, T., Peters, L., Pichens, R., Primus, E., Puill, L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Roychowdhury, T., Reite, M., Ruiz, S., Savary, G., Scherck, S., Scott, S., Shiu, J., Shu, J., Shu, J., Shu, J., Sisson, T., Sodergren, E., Sonakka, T., Sparks, A., Stanley, H., Strong, H., Sutton, A., Svatek, A., Taber, P., Tamerska, A., Tamerska, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vacquier, T., Varav, V., Villalobos, P., Vinsco, P., Watson, Q., Wanq, S., Ward-Moore, S., Warren, R., Washington, C., Williams, G., Williamson, J., Wlecyz, R., Woodson, S., Wren, J., Wu, C., Wu, Y., Wu, Y., Zhou, J., Zarritta, S., Nelson, D., Weinstock, G., and Gibbs, R.							
TITLE	Genome Center						
JOURNAL	Center code: BCM						
AUTHORS	Center : Baylor College of Medicine Center code: BCM						
COMMENT	Center : Baylor College of Medicine Center code: BCM						
1 (bases 1 to 187357)							
2 (bases 1 to 187357)							
TITLE	Direct Submission						
JOURNAL	Unpublished						
AUTHORS	Worley, K.C.						
COMMENT	Submitted (29-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA						
REFERENCE							
AUTHORS	Center : Baylor College of Medicine Center project name: GPKY Center cloud name: CH230-9GB						
COMMENT	Center : Baylor College of Medicine Center code: BCM Web site: http://www.hgsb.bcm.tmc.edu/ Contact: hgsb-help@bcm.tmc.edu Project Information Center project name: GPKY Center cloud name: CH230-9GB						
REFERENCE	Summary Statistics						

* NOTE: Estimated insert size may differ from sequencing
 * (see http://www.hgsb.bcm.edu/dna/Genbank_databank.html)
 * NOTE: This is a "working draft" sequence. It can never
 * consist of 65 contigs. The true order of the pieces
 * is not known and their order in this sequence is
 * arbitrary. Gaps between the contigs are represented
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number
 * be preserved.

Contig ID	Start Position	End Position	Length	Sequence
1	1046	1046	0	
1	1046	1146	100	gap of unknown length
1	1146	2240	1094	contig of 1354 bp in length
1	2240	2341	101	gap of unknown length
1	2341	3564	1223	contig of 1224 bp in length
1	3565	3655	90	gap of unknown length
1	3655	4830	1175	contig of 1156 bp in length
1	4830	4821	-1	gap of unknown length
1	4821	5965	1144	contig of 1045 bp in length
1	5965	6055	90	gap of unknown length
1	6055	6066	1	contig of 1033 bp in length
1	6066	7098	1032	contig of 1033 bp in length
1	7098	7198	100	gap of unknown length
1	7198	8391	1203	contig of 1192 bp in length
1	8391	8490	109	gap of unknown length
1	8490	10491	2001	contig of 2001 bp in length
1	10491	10591	100	gap of unknown length
1	10591	12309	1718	contig of 1718 bp in length
1	12310	12409	99	gap of unknown length
1	12410	13786	1377	contig of 1347 bp in length
1	13786	13857	71	gap of unknown length
1	13857	16065	2190	contig of 1613 bp in length
1	16066	16165	100	gap of unknown length
1	16165	1666	501	contig of 1705 bp in length
1	1666	17870	1213	gap of unknown length
1	17870	17930	60	contig of 1662 bp in length
1	17930	19812	1982	contig of 1662 bp in length
1	19812	19833	21	gap of unknown length
1	19833	21523	1690	contig of 1613 bp in length
1	21523	21543	20	gap of unknown length
1	21543	21562	19	contig of 1812 bp in length
1	21562	21643	81	contig of 1387 bp in length
1	21643	23454	1801	gap of unknown length
1	23454	23555	101	contig of 1668 bp in length
1	23555	23573	18	gap of unknown length
1	23573	25323	1750	contig of 1851 bp in length
1	25323	27173	1850	gap of unknown length
1	27173	27274	101	contig of 1387 bp in length
1	27274	28660	1196	gap at unknown length
1	28660	28760	100	contig of 1261 bp in length
1	28760	30021	1341	contig of 1752 bp in length
1	30021	30122	101	gap of unknown length
1	30122	31325	1223	contig of 1204 bp in length
1	31325	31425	100	gap of unknown length
1	31425	31426	1	contig of 1662 bp in length
1	31426	32887	1461	contig of 1680 bp in length
1	32887	32997	110	gap of unknown length
1	32997	32988	9	contig of 1752 bp in length
1	32988	34740	1752	contig of unknown length
1	34740	34849	109	gap of unknown length
1	34849	36605	1756	contig of 1656 bp in length
1	36605	36696	91	gap of unknown length
1	36696	36795	100	contig of 2485 bp in length
1	36795	36920	125	contig of 1680 bp in length
1	36920	37481	581	gap of unknown length
1	37481	39310	1929	contig of 1330 bp in length
1	39310	40710	1400	contig of 1574 bp in length
1	40710	40811	101	gap of unknown length
1	40811	42412	1611	contig of 1682 bp in length
1	42412	42593	881	gap of unknown length
1	42593	42553	62	contig of 1680 bp in length
1	42553	44212	1473	contig of unknown length
1	44212	44373	66	gap of unknown length
1	44373	45956	1437	contig of 1574 bp in length
1	45956	46046	9	gap of unknown length

ACCESSION	AC-094597
VERSION	AC-094597.3
REFERENCE	Gl:21716297
AUTHORS	
KEYWORDS	HIV; HIV-KASEL;
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Monotria; Rattus; Rattus rattus	
• 57986; contig of 1844 bp in length	57986; gap of unknown length
• 56071; gap of 2286 bp in length	56071; gap of unknown length
• 56172; contig of 2017 bp in length	56172; gap of unknown length
• 58188; contig of 1917 bp in length	58188; gap of unknown length
• 59007; contig of 3678 bp in length	59007; gap of unknown length
• 59485; contig of 1153 bp in length	59485; gap of unknown length
• 60315; gap of unknown length	60315; gap of unknown length
• 60615; contig of 2440 bp in length	60615; gap of unknown length
• 61054; contig of 2226 bp in length	61054; gap of unknown length
• 61215; contig of 1579 bp in length	61215; gap of unknown length
• 64734; contig of 1661 bp in length	64734; gap of unknown length
• 64844; contig of 1153 bp in length	64844; gap of unknown length
• 65993; contig of 2441 bp in length	65993; gap of unknown length
• 66093; contig of 2441 bp in length	66093; gap of unknown length
• 68544; contig of 2536 bp in length	68544; gap of unknown length
• 71170; contig of 1579 bp in length	71170; gap of unknown length
• 71279; contig of 1661 bp in length	71279; gap of unknown length
• 72941; contig of 2441 bp in length	72941; gap of unknown length
• 73031; contig of 2681 bp in length	73031; gap of unknown length
• 75011; contig of 2681 bp in length	75011; gap of unknown length
• 78812; contig of 3042 bp in length	78812; gap of unknown length
• 78854; contig of 2175 bp in length	78854; gap of unknown length
• 78954; contig of 4011 bp in length	78954; gap of unknown length
• 81228; contig of 3121 bp in length	81228; gap of unknown length
• 81229; contig of 2916 bp in length	81229; gap of unknown length
• 84145; contig of 1642 bp in length	84145; gap of unknown length
• 84245; contig of 3864 bp in length	84245; gap of unknown length
• 85887; contig of 2524 bp in length	85887; gap of unknown length
• 88998; contig of 3236 bp in length	88998; gap of unknown length
• 89098; contig of 4555 bp in length	89098; gap of unknown length
• 92119; contig of 4371 bp in length	92119; gap of unknown length
• 96183; contig of 3236 bp in length	96183; gap of unknown length
• 107033; contig of 4375 bp in length	107033; gap of unknown length
• 110269; contig of 4402 bp in length	110269; gap of unknown length
• 111770; contig of 3739 bp in length	111770; gap of unknown length
• 113871; contig of 4190 bp in length	113871; gap of unknown length
• 117610; contig of 4361 bp in length	117610; gap of unknown length
• 122071; contig of 4375 bp in length	122071; gap of unknown length
• 122711; contig of 4375 bp in length	122711; gap of unknown length
• 126546; contig of 4375 bp in length	126546; gap of unknown length
• 126646; contig of 4375 bp in length	126646; gap of unknown length
• 130846; contig of 4375 bp in length	130846; gap of unknown length
• 74948; GTCATTAATTTTCTTACAGG 7516	
QIOTY MATCH	7.4.8%
HOST LIGAND SIMILARITY	87.5%
MATCHES	21;
REFERENCE	Conserve190
COMMENT	4 GRIN TAATTTCCTTACAGG 26
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 193446)
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (15-Sep-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, one Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 193446)
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (10-Jun-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, one Baylor Plaza, Houston, TX 77030, USA
COMMENT	on Jul 9, 2002 this sequence version replaced q1.17941361. Genome Center
Center: Baylor College of Medicine	

Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: phrap; version 0.990329
Consensus quality: 9683 bases at least Q40
Consensus quality: 103408 bases at least Q30
Consensus quality: 107911 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length.
* (see <http://www-lgs.tum.de/~dbs/standards/draft.html>)
* NOTE: This is a 'working draft' sequence; it currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
be preserved.

1 1664: contig of 1664 bp in length
* 1665 1764: gap of unknown length
* 1765 3115: contig of 1351 bp in length
* 3116 3215: gap of unknown length
* 3220: contig of 1005 bp in length
* 4221 4220: gap of unknown length
* 4321 5450: contig of 1130 bp in length
* 5451 5550: gap of unknown length
* 5551 6821: contig of 1771 bp in length
* 6822 6922: gap of unknown length
* 8122 8421: gap of unknown length
* 8422 9512: gap of unknown length
* 9512 10708: contig of 1186 bp in length
* 10708 10998: gap of unknown length
* 10899 12339: contig of 1341 bp in length
* 12240 12339: gap of unknown length
* 12410 13160: contig of 1091 bp in length
* 13160 13454: gap of unknown length
* 13454 14660: contig of 1401 bp in length
* 14660 14861: gap of unknown length
* 14861 14961: contig of 1612 bp in length
* 14961 16573: gap of unknown length
* 16573 17751: contig of 1079 bp in length
* 17752 18551: gap of unknown length
* 18551 19156: contig of 1305 bp in length
* 19156 19256: gap of unknown length
* 19256 20442: contig of 1186 bp in length
* 20442 20443: gap of unknown length
* 20443 21771: contig of 1128 bp in length
* 21771 21873: gap of unknown length
* 21873 21871: contig of 1106 bp in length
* 21871 23136: gap of unknown length
* 23137 24364: contig of 1228 bp in length
* 24364 24465: gap of unknown length
* 24465 25865: contig of 1401 bp in length
* 25865 25965: gap of unknown length
* 25965 25967: contig of 1002 bp in length
* 25967 27167: gap of unknown length
* 27167 27068: contig of 1210 bp in length
* 27068 28403: gap of unknown length
* 28403 28503: contig of 1085 bp in length
* 28503 29581: gap of unknown length
* 29581 29881: contig of 1188 bp in length
* 29881 30868: gap of unknown length
* 30868 30969: contig of 1232 bp in length
* 30969 32178: gap of unknown length
* 32178 32279: contig of 1085 bp in length
* 32279 33163: gap of unknown length
* 33163 3364: gap of unknown length
* 3364 34925: contig of 1462 bp in length
* 34925 35026: gap of unknown length
* 35026 36258: contig of 1616 bp in length
* 36258 37973: contig of 1516 bp in length
* 37973: gap of unknown length

Query Match
Best Local Similarity: 87.5%; Pred. NG: 2.5e+02;
Matches: 21; Conservative: 0; Mismatches: 3; Index: 0; Gaps: 0;

Oy 3 GTCCTAATCTTCTCGGTACACC 26
LU TATGGGTTAAACGTTTGAGCAAG 73070

Search completed: January 14 2003, 14:04:38
Job time : 383.313 secs

